

U.S. Patent Application No. 10/611,414
Amendment and Reply dated November 25, 2008
In Response to Office Action dated October 14, 2008

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AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently Amended) A method for allelic classification, the method comprising:
providing a system comprising a sample processing component and a data analysis component;

acquiring intensity information from the sample processing component, for each of a plurality of samples wherein the intensity information for each sample of the plurality of samples comprises a first intensity component representing the detected emission of a first probe specific for a first allele of a gene and a second intensity component representing the detected emission of a second probe specific for a second allele of the gene;

forming a plurality of data sets from the intensity information, such that each data set comprises the first intensity component and the second intensity component from a respective one of the plurality of samples;

grouping the plurality of data sets into one or more data clusters by evaluating at least the relationship between the first intensity component and the second intensity component for each of the plurality of samples, wherein each data cluster represents a discrete allelic classification comprising one of, a homozygous allelic combination comprising the first allele alone, a homozygous allelic combination comprising the second allele alone, or a heterozygous allelic combination comprising both the first allele and the second allele;

defining bounds for each of the one or more data clusters;

generating a likelihood model that predicts the probability that an allelic combination of a

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selected sample from the plurality of samples will reside within the bounds of a particular data cluster of the one or more data clusters, based upon the intensity information of the selected sample;

applying the likelihood model to the intensity information of each of the plurality of samples to identify the allelic classification of each sample of the plurality of samples; and

outputting the allelic classification of each of the plurality of samples to at least one of a user and a display component;

wherein the data analysis component performs at least one of the steps of forming, grouping, defining, generating, and applying.

2. (Original) The method of claim 1, wherein the likelihood model comprises a model-fit probability assessment that estimates confidence in the likelihood model itself and assesses how well a selected sample and its respective intensity information fit the model.

3. (Original) The method of claim 1, wherein the likelihood model comprises an in-class probability assessment that estimates the probability that a selected cluster identifies a selected sample and its respective intensity information.

4. (Original) The method of claim 1, wherein the likelihood model comprises an a posteriori probability assessment that estimates the probability of a selected sample and its respective intensity information belonging to an assigned cluster.

5. (Previously presented) The method of claim 1, wherein the one or more data clusters

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comprise at least three discrete data clusters each associated with a different combination selected from neither the first allele nor the second allele, the first allele alone, the second allele alone, and both the first allele and the second allele.

6. (Previously presented) The method of claim 1, wherein the at least one data cluster comprises a cluster representing a first homozygous allelic classification.
7. (Previously presented) The method of claim 1, wherein the at least one data cluster comprises a cluster representing a first heterozygous allelic classification.
8. (Previously presented) The method of claim 1, wherein the at least one data cluster comprises a cluster representing a second homozygous allelic classification.
9. (Original) The method of claim 1, wherein the allelic classification is used to perform a mutational analysis of one or more samples.
10. (Original) The method of claim 1, wherein the allelic classification is used to perform a single nucleotide polymorphism analysis of one or more samples.
11. (Previously presented) The method of claim 1, wherein a genotype for one or more samples is identified by performing the allelic classification.
12. (Previously presented) The method of claim 1, wherein the intensity information for the

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plurality of samples is normalized.

13. (Previously presented) The method of claim 1, wherein the plurality of samples comprise at least one control sample and associated intensity information that is used for the purposes of sample scaling.

14. (Original) The method of claim 1, wherein the likelihood model is generated in an iterative manner to refine the likelihood model.

15. (Original) The method of claim 14, wherein two or more iterations are used to generate a refined likelihood model.

16. (Canceled)

17. (Original) The method of claim 14, wherein refinement of the likelihood model comprises performing a data resampling operation wherein a subset of the plurality of samples are used to generate the refined likelihood model.

18. (Canceled)

19. (Previously presented) The method of claim 1, wherein the intensity information for each sample is acquired from an amplification protocol.

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20. (Previously presented) The method of claim 19, wherein the amplification protocol comprises a Taqman or SNplex protocol.

21. (Original) The method of claim 1, wherein the intensity information for each sample is acquired from an array-based detection protocol.

22.-83. (Canceled)

84. (Previously Presented) The method of claim 1, further comprising acquiring a plot of the intensity information, the plot comprising a first axis corresponding to the first intensity component and a second axis corresponding to the second intensity component.

85. (Previously Presented) The method of claim 84, wherein the one or more data clusters each comprise groupings of data points defined by the first intensity component and the second intensity component in a discrete area of the plot.

86. (New) The method of claim 1, wherein the data analysis component performs the step of forming.

87. (New) The method of claim 1, wherein the data analysis component performs the step of grouping.

88. (New) The method of claim 1, wherein the data analysis component performs the step of

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defining.

89. (New) The method of claim 1, wherein the data analysis component performs the step of generating.

90. (New) The method of claim 1, wherein the data analysis component performs the step of applying.